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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/635,501

DATE: 08/17/2000
 TIME: 10:09:55

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\08162000\I635501.raw

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3 <110> APPLICANT: Acton, Susan L. et al.
 5 <120> TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
 6 DIAGNOSTIC USES THEREFOR
 8 <130> FILE REFERENCE: MNI-132CP3
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/635,501
 C--> 11 <141> CURRENT FILING DATE: 2000-08-09
 13 <150> PRIOR APPLICATION NUMBER: 09/407,427
 14 <151> PRIOR FILING DATE: 1999-09-29
 16 <150> PRIOR APPLICATION NUMBER: 09/163,648
 17 <151> PRIOR FILING DATE: 1998-09-30
 19 <150> PRIOR APPLICATION NUMBER: 08/989,299
 20 <151> PRIOR FILING DATE: 1997-12-11
 22 <160> NUMBER OF SEQ ID NOS: 107
 24 <170> SOFTWARE: PatentIn Ver. 2.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3396
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (82)..(2496)
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 38 tatcttggtt cacaggggac g atg tca agc tct tcc tgg ctc ctt ctc agc 111
 39 Met Ser Ser Ser Ser Trp Leu Leu Leu Ser
 40 1 5 10
 42 ctt gtt gct gta act gct gct cag tcc acc att gag gaa cag gcc aag 159
 43 Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys
 44 15 20 25
 46 aca ttt ttg gac aag ttt aac cac gaa gcc gaa gac ctg ttc tat caa 207
 47 Thr Phe Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu Phe Tyr Gln
 48 30 35 40
 50 agt tca ctt gct tct tgg aat tat aac acc aat att act gaa gag aat 255
 51 Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn
 52 45 50 55
 54 gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc ttt tta aag 303
 55 Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys
 56 60 65 70
 58 gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa att cag aat 351
 59 Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn
 60 75 80 85 90
 62 ctc aca gtc aag ctt cag ctg cag gct ctt cag caa aat ggg tct tca 399
 63 Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser
 64 95 100 105
 66 gtg ctg tca gaa gac aag agc aaa cgg ttg aac aca att cta aat aca 447
 67 Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr
 68 110 115 120

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70 atg agc acc atc tac agt act gga aaa gtt tgt aac cca gat aat cca 495
71 Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro Asp Asn Pro
72      125      130      135
74 caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata atg gca aac 543
75 Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile Met Ala Asn
76      140      145      150
78 agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc tgg aga tct 591
79 Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser
80 155      160      165      170
82 gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat gtg gtc ttg 639
83 Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu
84      175      180      185
86 aaa aat gag atg gca aga gca aat cat tat gag gac tat ggg gat tat 687
87 Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr
88      190      195      200
90 tgg aga gga gac tat gaa gta aat ggg gta gat ggc tat gac tac agc 735
91 Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser
92      205      210      215
94 cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa gag att aaa 783
95 Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu Glu Ile Lys
96      220      225      230
98 cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag ttg atg aat 831
99 Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys Leu Met Asn
100 235      240      245      250
102 gcc tat cct tcc tat atc agt cca att gga tgc ctc cct gct cat ttg 879
103 Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro Ala His Leu
104      255      260      265
106 ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac tct ttg aca 927
107 Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr
108      270      275      280
110 gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat gca atg gtg 975
111 Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp Ala Met Val
112      285      290      295
114 gac cag gcc tgg gat gca cag aga ata ttc aag gag gcc gag aag ttc 1023
115 Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe
116      300      305      310
118 ttt gta tct gtt ggt ctt cct aat atg act caa gga ttc tgg gaa aat 1071
119 Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe Trp Glu Asn
120 315      320      325      330
122 tcc atg cta acg gac cca gga aat gtt cag aaa gca gtc tgc cat ccc 1119
123 Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val Cys His Pro
124      335      340      345
126 aca gct tgg gac ctg ggg aag ggc gac ttc agg atc ctt atg tgc aca 1167
127 Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu Met Cys Thr
128      350      355      360
130 aag gtg aca atg gac gac ttc ctg aca gct cat cat gag atg ggg cat 1215
131 Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu Met Gly His
132      365      370      375
134 atc cag tat gat atg gca tat gct gca caa cct ttt ctg cta aga aat 1263

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135 Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn
136      380      385      390
138 gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc atg tca ctt 1311
139 Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile Met Ser Leu
140 395      400      405      410
142 tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt ctg tca ccc 1359
143 Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu Leu Ser Pro
144      415      420      425
146 gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg ctc aaa caa 1407
147 Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln
148      430      435      440
150 gca ctc acg att gtt ggg act ctg cca ttt act tac atg tta gag aag 1455
151 Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys
152      445      450      455
154 tgg agg tgg atg gtc ttt aaa ggg gaa att ccc aaa gac cag tgg atg 1503
155 Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp Gln Trp Met
156      460      465      470
158 aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg gtg gaa cct 1551
159 Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val Val Glu Pro
160 475      480      485      490
162 gtg ccc cat gat gaa aca tac tgt gac ccc gca tct ctg ttc cat gtt 1599
163 Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu Phe His Val
164      495      500      505
166 tct aat gat tac tca ttc att cga tat tac aca agg acc ctt tac caa 1647
167 Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln
168      510      515      520
170 ttc cag ttt caa gaa gca ctt tgt caa gca gct aaa cat gaa ggc cct 1695
171 Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His Glu Gly Pro
172      525      530      535
174 ctg cac aaa tgt gac atc tca aac tct aca gaa gct gga cag aaa ctg 1743
175 Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu
176      540      545      550
178 ttc aat atg ctg agg ctt gga aaa tca gaa ccc tgg acc cta gca ttg 1791
179 Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu
180 555      560      565      570
182 gaa aat gtt gta gga gca aag aac atg aat gta agg cca ctg ctc aac 1839
183 Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro Leu Leu Asn
184      575      580      585
186 tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac aag aat tct 1887
187 Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser
188      590      595      600
190 ttt gtg gga tgg agt acc gac tgg agt cca tat gca gac caa agc atc 1935
191 Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile
192      605      610      615
194 aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa gca tat gaa 1983
195 Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu
196      620      625      630
198 tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt gca tat gct 2031
199 Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala

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200 635          640          645          650
202 atg agg cag tac ttt tta aaa gta aaa aat cag atg att ctt ttt ggg 2079
203 Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile Leu Phe Gly
204          655          660          665
206 gag gag gat gtg cga gtg gct aat ttg aaa cca aga atc tcc ttt aat 2127
207 Glu Glu Asp Val Arg Val Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn
208          670          675          680
210 ttc ttt gtc act gca cct aaa aat gtg tct gat atc att cct aga act 2175
211 Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile Pro Arg Thr
212          685          690          695
214 gaa gtt gaa aag gcc atc agg atg tcc cgg agc cgt atc aat gat gct 2223
215 Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile Asn Asp Ala
216          700          705          710
218 ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata cag cca aca 2271
219 Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr
220 715          720          725          730
222 ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg att gtt ttt 2319
223 Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu Ile Val Phe
224          735          740          745
226 gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc ctg atc ttc 2367
227 Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile Leu Ile Phe
228          750          755          760
230 act ggg atc aga gat cgg aag aag aaa aat aaa gca aga agt gga gaa 2415
231 Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu
232          765          770          775
234 aat cct tat gcc tcc atc gat att agc aaa gga gaa aat aat cca gga 2463
235 Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly
236          780          785          790
238 ttc caa aac act gat gat gtt cag acc tcc ttt tagaaaaatc tatgtttttc 2516
239 Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
240 795          800          805
242 ctcttgaggt gattttgttg tatgtaaatg ttaatttcat ggtatagaaa atataagatg 2576
244 ataaagatat cattaaatgt caaaactatg actctgttca gaaaaaaaat tgtccaaaga 2636
246 caacatggcc aaggagagag catcttcatt gacattgctt tcagtattta tttctgtctc 2696
248 tggatttgac ttctgttctg ttctttaata aggattttgt attagagtat attagggaaa 2756
250 gtgtgtattt ggtctcacag gctgttcagg gataatctaa atgtaaatgt ctgttggaatt 2816
252 tctgaagttg aaaacaagga tatatcattg gagcaagtgt tggatcttgt atggaatatg 2876
254 gatggatcac ttgtaaggac agtgcctggg aactgggtga gctgcaagga ttgagaatgg 2936
256 catgcattag ctcaacttca tttaattccat tgtcaaggat gacatgcttt ctccacagta 2996
258 actcagttca agtactatgg tgatttgctt acagtgatgt ttggaatcga tcatgctttc 3056
260 ttcaaggtga cagggtctaaa gagagaagaa tccaggggaa aggtagagga cattgctttt 3116
262 tcaacttcaa ggtgcttgat caacatctcc ctgacaacac aaaactagag ccaggggcct 3176
264 ccgtgaactc ccagagcatg cctgatagaa actcatttct actgttctct aactgtggag 3236
266 tgaatggaaa ttccaactgt atgttcaccc tctgaagtgg gtacccagtc tcttaaatct 3296
268 tttgtatttg ctacacagtgt ttgagcagtg ctgagcacia agcagacact caataaatgc 3356
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273 <210> SEQ ID NO: 2
274 <211> LENGTH: 805
275 <212> TYPE: PRT

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283   20           25           30
285 Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
286   35           40           45
288 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
289   50           55           60
291 Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
292   65           70           75           80
294 Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln
295   85           90           95
297 Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
298   100          105          110
300 Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
301   115          120          125
303 Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu
304   130          135          140
306 Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu
307  145          150          155          160
309 Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu
310   165          170          175
312 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
313   180          185          190
315 Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
316   195          200          205
318 Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu
319   210          215          220
321 Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu
322  225          230          235          240
324 His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile
325   245          250          255
327 Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
328   260          265          270
330 Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
331   275          280          285
333 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
334   290          295          300
336 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
337  305          310          315          320
339 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
340   325          330          335
342 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
343   340          345          350
345 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
346   355          360          365
348 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date